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CCEPTED MANUSCRIPT

Identification on novel locus of dairy traits of Kazakh horse in Xinjiang

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ABSTRACT

The utility of high-density single nucleotide polymorphism (SNP) data help to accurately identify

genomic regions that have undergone positive selection. In this study, the Affymetrix Equine 670K

high-density SNP array was used to genotype Kazakh and Yili horse population. After quality

control, 370,227 autosomal SNPs were used to detect selection signatures by using global fixation

index  $(F_{ST})$  and cross-population extended haplotype homozygosity (XP-EHH). The database of

Ensemble, Genecards, and NCBI were used to make gene annotation and functional analysis. The

results showed that there were 134 candidate SNPs overlapped between  $F_{\rm ST}$  and XP-EHH in

Kazakh horse. We also discovered some potential selective sweep regions associated with milk

trait, including NUMB, LGALS2, ADCY8, SLC25A30, and CA8 genes. New findings from this

research has potential value for milk traits selecting in horse.

Keywords:  $F_{ST}$ ; XP-EHH; selection; Kazakh horse; Yili horse

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1. Introduction

Domestication is a long-term process for animal adapting to environment, artificial selection

can render tremendous changes to animal behavior, body size, and some important traits together

with domestication progress [1-2]. Horse were domesticated approximately 5,000 years ago [3-5]. In

the past 400 years, the founding of formal breed registries and subsequent breed specialization has

focused more upon preserving and improving traits related to aesthetics and performance <sup>[6]</sup>. With

the rapid development of society, the use of horses for transportation, warfare, and agriculture has

resulted in diverse populations distributed across the world. The racing line of Quarter horse was

characterized by great sprinting speed over short distances on straight tracks [7]. Swedish

warmblood riding horses were used for riding, and 4-year-old horses of both genders could

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